

FIG. 1

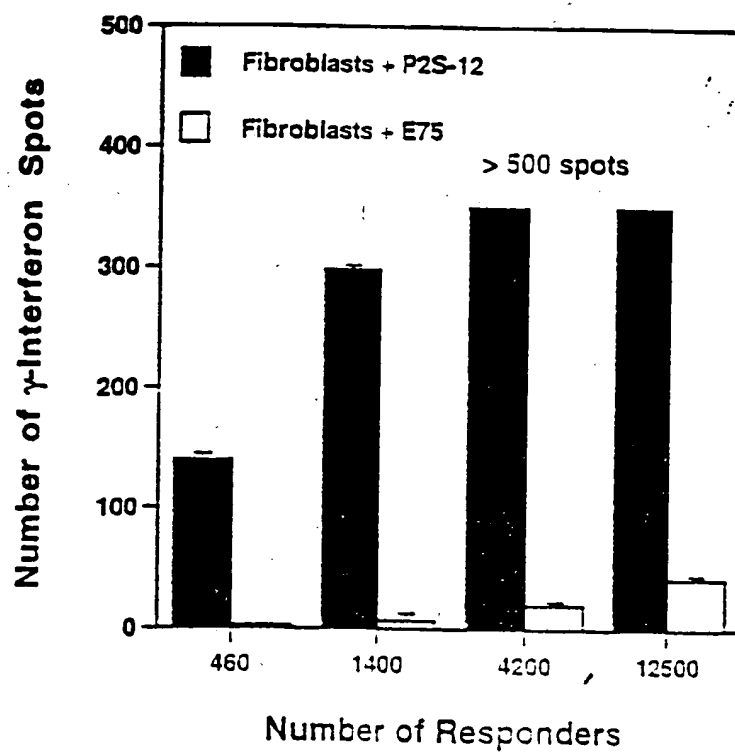
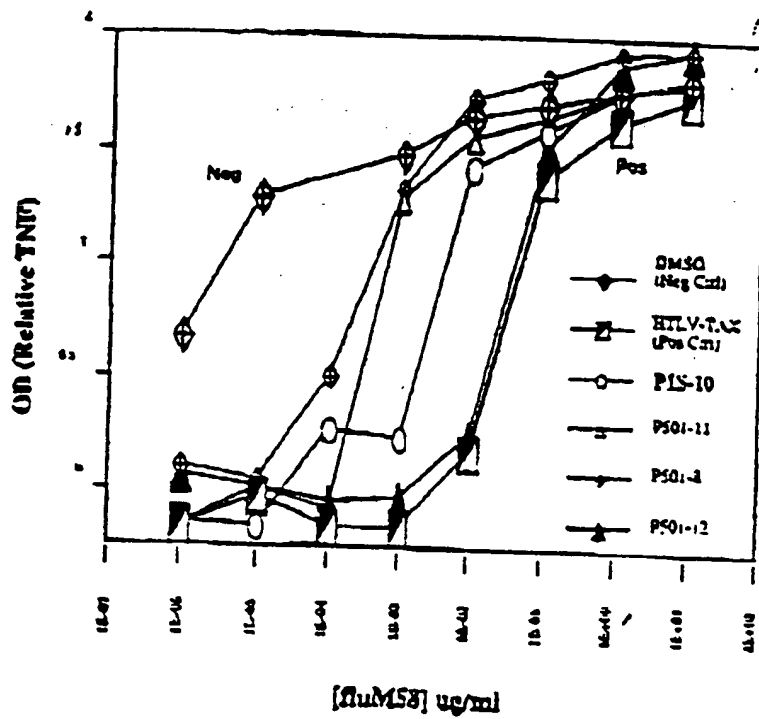


FIG. 2A

A bar chart comparing the number of γ -interferon spots for two cell lines: Fibroblasts / P502S (black bars) and Fibroblasts / HER-2 (white bars). The x-axis represents the 'Number of Responders' with categories 460, 1400, 4200, and 12500. The y-axis represents the 'Number of γ -Interferon Spots' ranging from 0 to 125. Error bars are present on all bars.

Number of Responders	Fibroblasts / P502S (Spots)	Fibroblasts / HER-2 (Spots)
460	~5	~2
1400	~15	~1
4200	~58	~10
12500	~95	~28

FIG. 2B



Figure

3

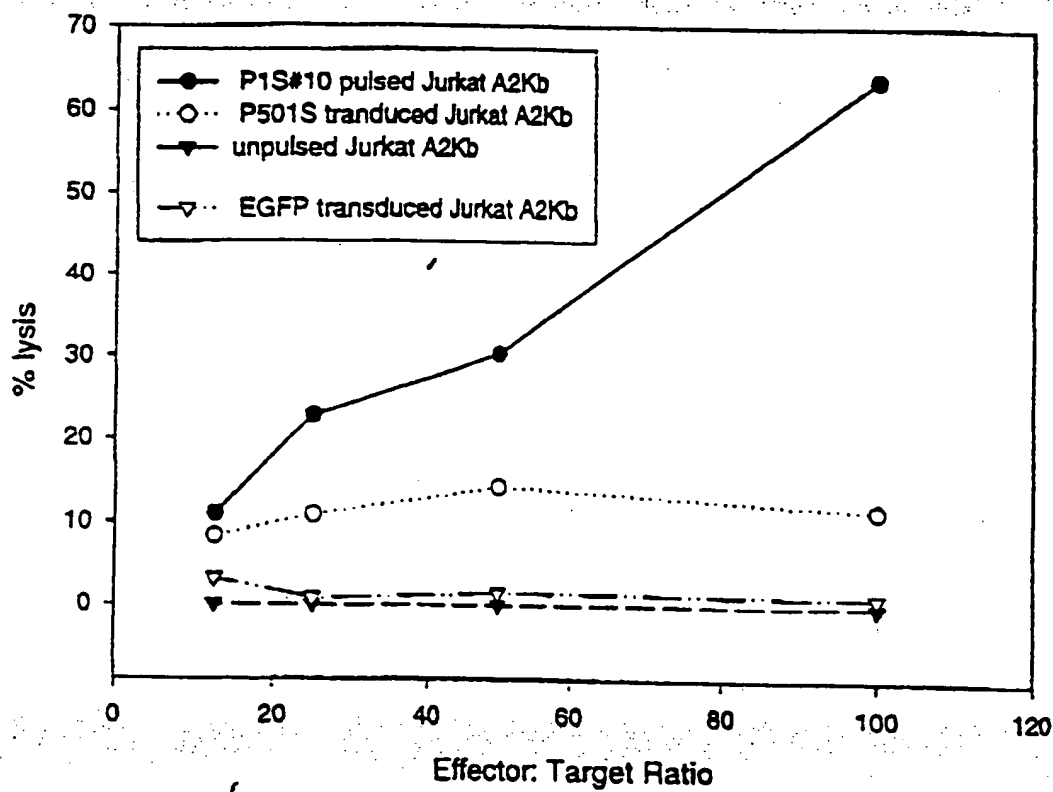


Figure 4

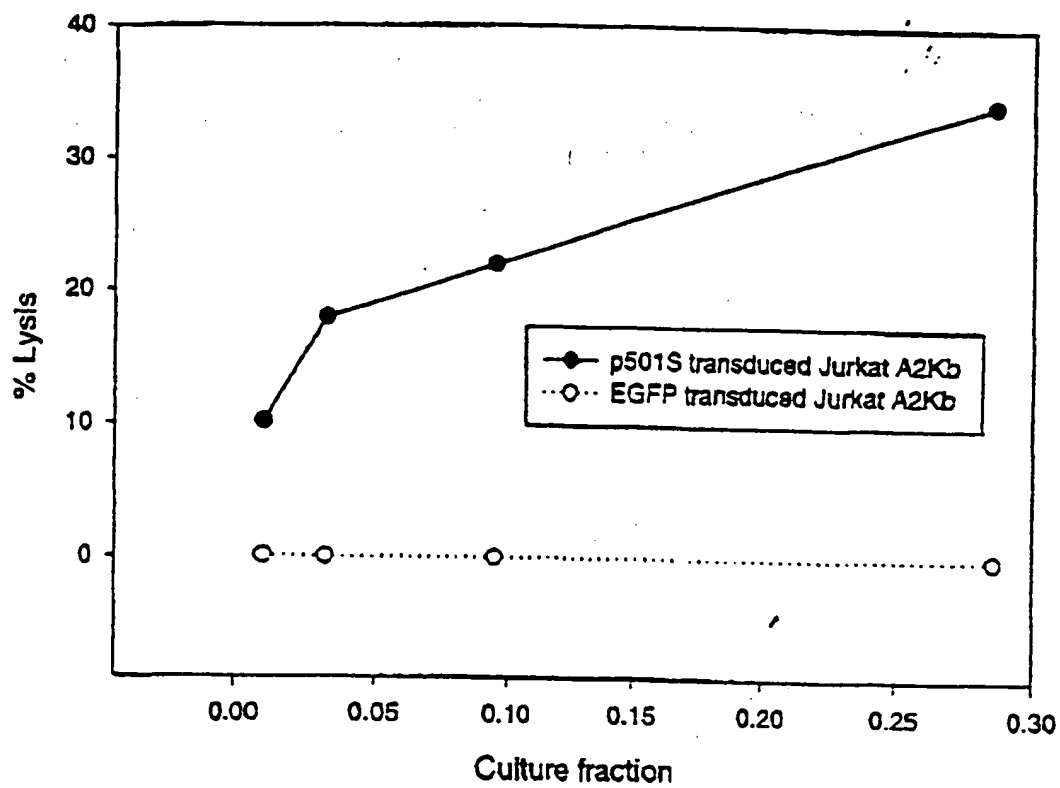


Figure 5

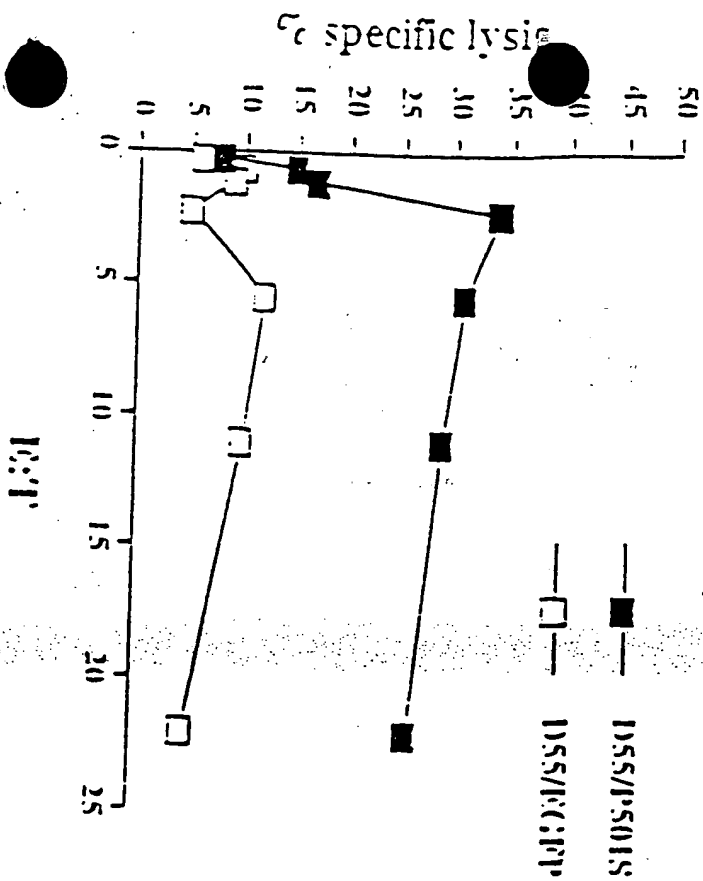


Fig. 6A

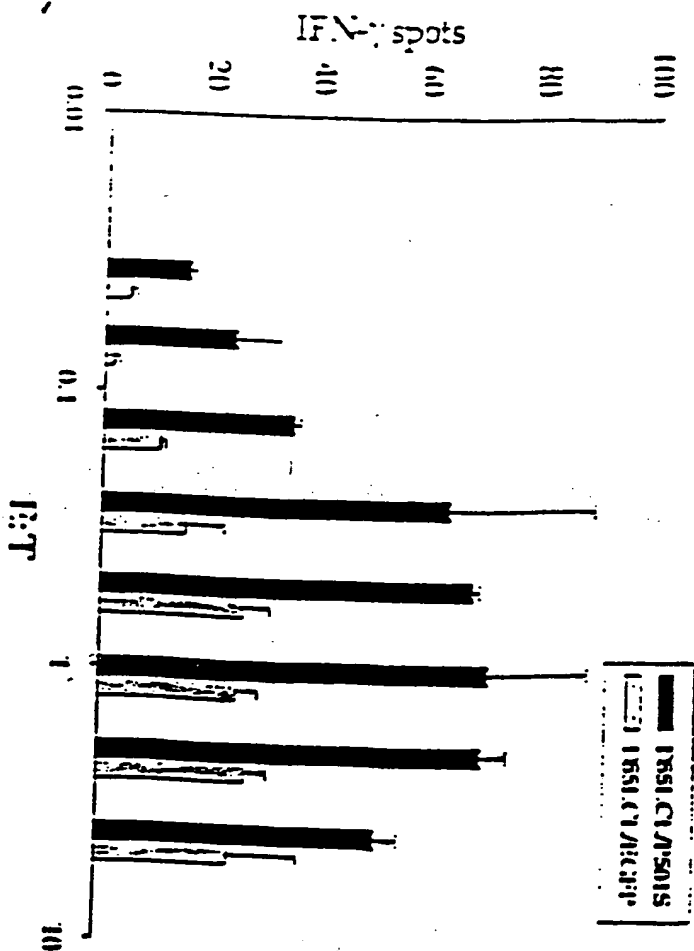
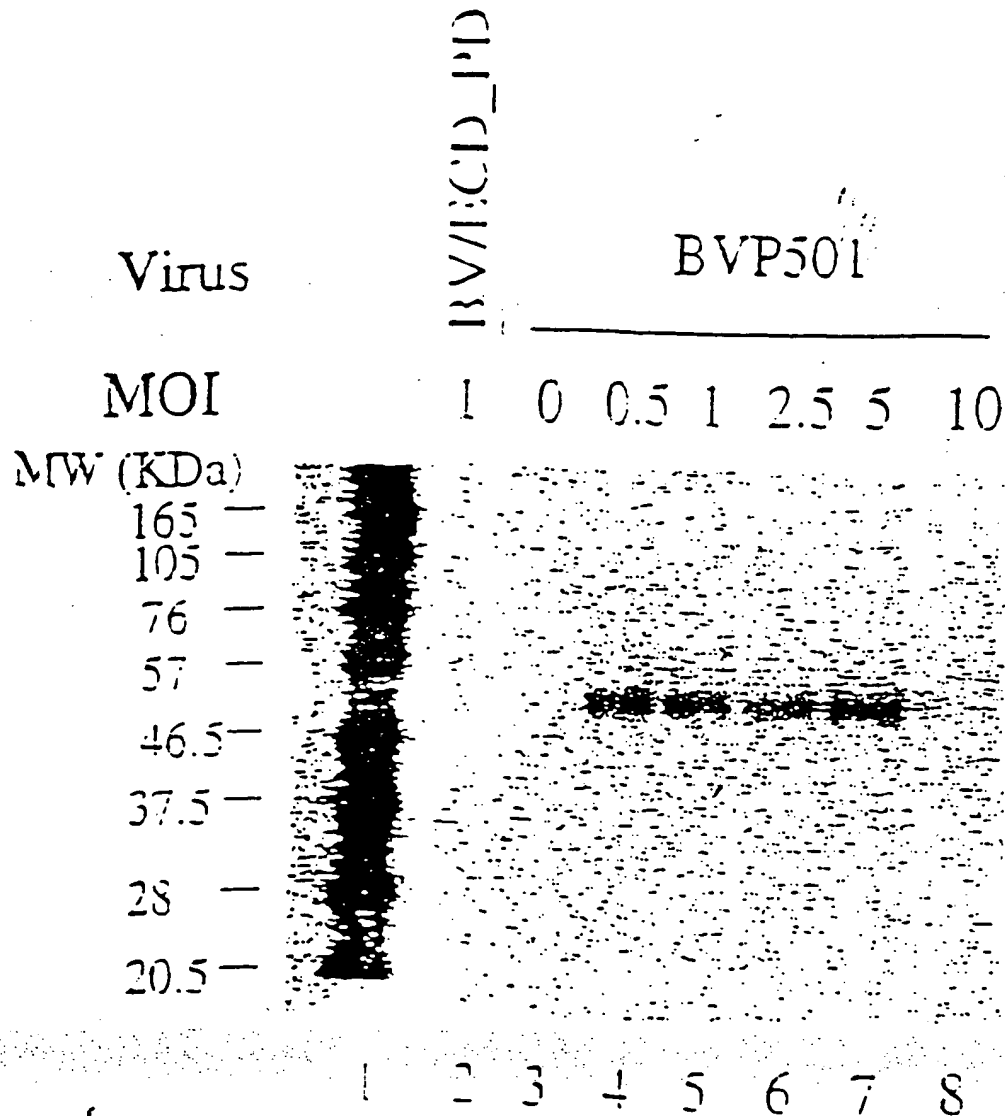


Fig. 6B

Expression of P501S by the Baculovirus Expression System



0.6 million high cells in 6-well plate were infected with an unrelated control virus BV/ECD_PC (lanes 1-3) without virus (lane 2), or with recombinant baculovirus for P501S at different MOIs (lane 4-8). Cell lysates were run on SDS-PAGE under the reducing conditions and analysed by Western blot with a monoclonal antibody against P501S-ICED-GAD65. Lane 1 is the bioanalytical protein molecular weight marker (kDa).

Fig. 7

7

Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

MVQRAVSVLRIRK AGLLYNLLTGLEVCLAACTVYVPLLRVGVVERKFM TNYLQIGPYLQLYCYPLLSAS
 DWWRGRYGRRRP EWALSLQILSLFLPRAGWL AGLCTDPRPLLE LAIILQVGLLDFCQGVCTPL
 FALSLDFRDPDHCRR AYSVYAFEMISLGGCTGVLPAL DWVTSALAPVLCQDRE
 CLPGLTLFLTCYAAATLY AFEAACTPEPARGASPSPICTP RARLAFRNIGAILPRI
 HOLCTAMPRTLR LPYAFCTYWMALMTFLTYTP VGEGLYQGVPRAPPTEARRIYDEGYR
 MGLGLFLQCAISLYSLYM DRIVQREFCTRAVYAS VAAFPYAACIATCLSHSVAVYTA SAA
 LTGETTSALQILTYTLASLY HREKQVFLPKYRGDTGASSEDSIMTSELP GPKPGAPFPNCHIVGAGGSL
 LPPPPALCGASACDVSVRVVGEPTEARVVPVGRG ICLDLAHLPSAFLSQVAPSLF MGSIVQLSQS
 VTAYMVSAAGLILYALYFAT QVVFDSDLAKYSA

Underlined sequence: Predicted transmembrane domain; Bold sequence: Predicted extracellular domain;
 Italic sequence: Predicted intracellular domain. Sequence in bold/underlined: used to generate polyclonal rabbit serum

Localization of domains predicted using IMMTOPI (G.F. Tusnady and I. Simon (1998) Principles
 Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction. J.Mol Biol. 283,
 489-506.

Genomic Map of (5) Corlxa Candidate Genes

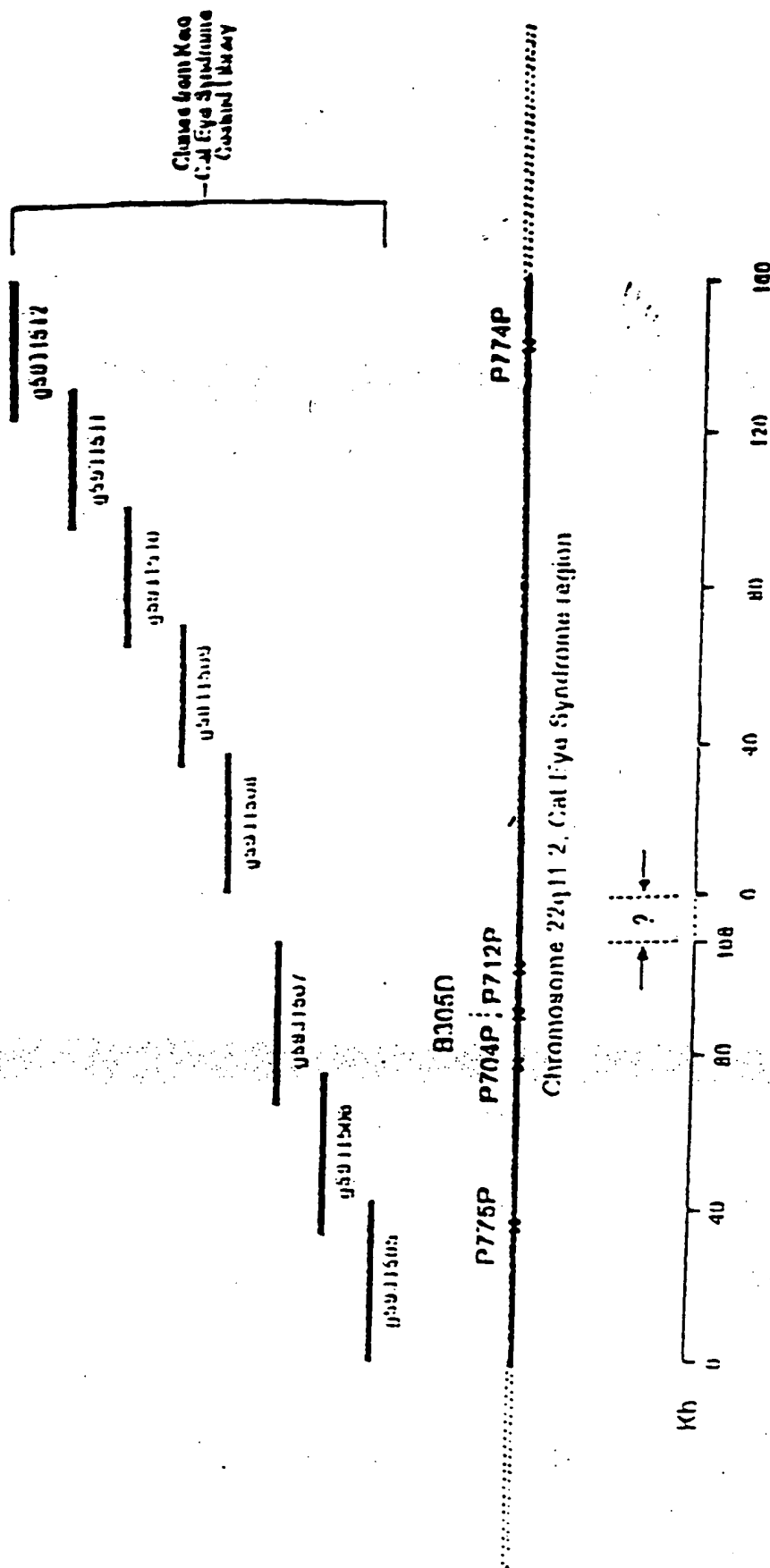


Fig. 10

FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity

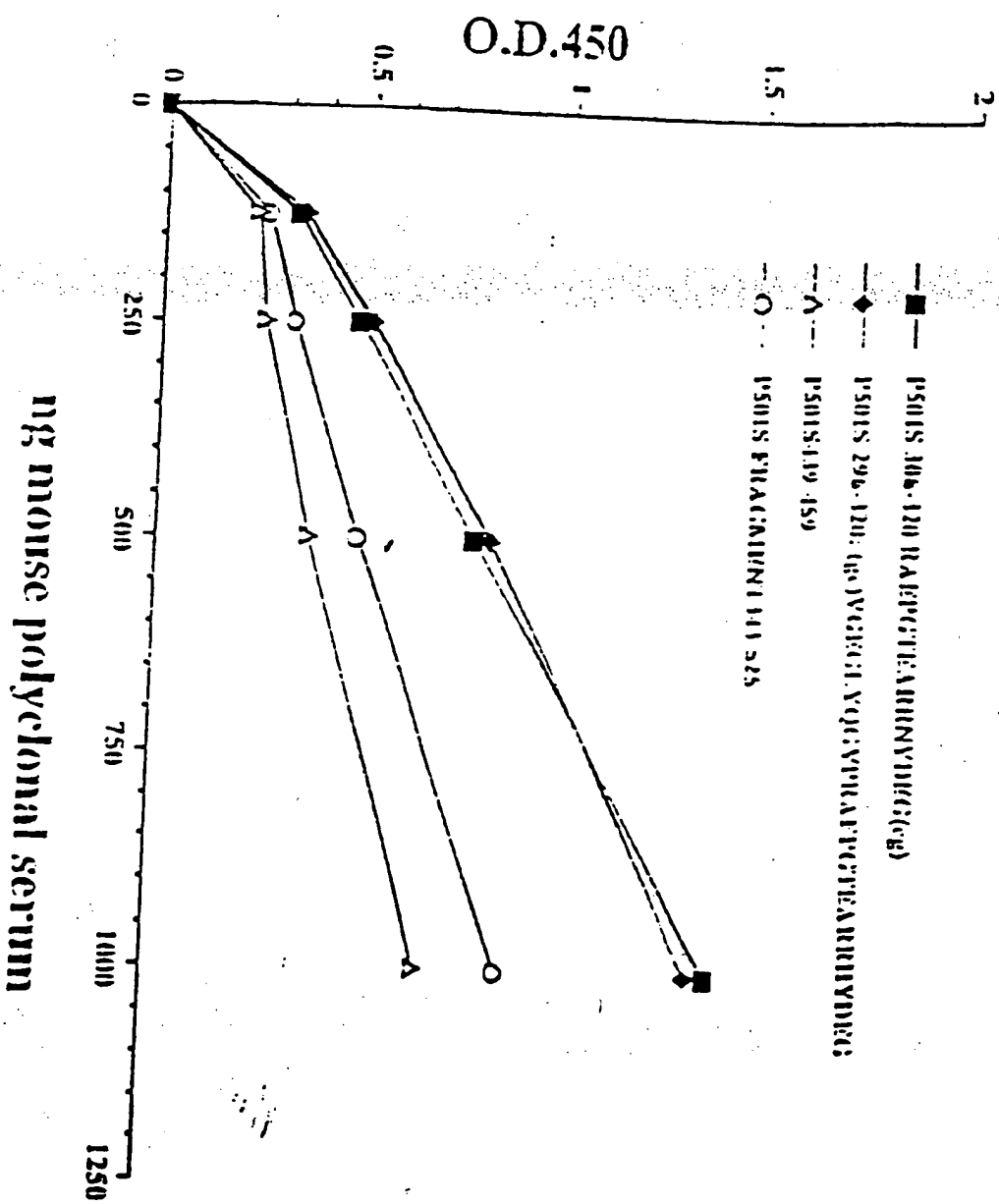


Fig. 11

00592793-054300

10 20 30 40 50 60 70

GTCACCTAGGAAAAGGTGTCTTTTCGGGCAGCCGGGCTCAGCATGAGGAACAGAAGGAATGACACTCTGG 70
ACAGCACCCGGACCCTGTACTCCAGCGCGTCTCGGAGCACAGACTTGTCTTACACTGAAAGCGACTTGGT 140
GAATTTTATTCAAGCAAATTTTAAGAAACGAGAATGTGTCTTCTTTACCAAAGATTCCAAGGCCACGGAG 210
AATGTGTGCAAGTGTGGCTATGCCAGAGCCAGCAGATGGAAGGCACCCAGATCAACCAAAGTGAGAAAT 280
GGAAGTACAAGAAACACACCAAGGAATTTCTACCGACGCCTTTGGGGATATTTCAGTTTGAGACACTGGG 350

360 370 380 390 400 410 420

GAAGAAAGGGAAGTATATACGTCTGTCTTGCAGACAGGACGCGGAAATCCTTTACGAGCTGCTGACCCAG 420
CACTGGCAGCTGAAAACAACCAACCTGGTCATTTCTGTGACCGGGGGCGCCAAGAAGTTGCGCCTGAAGC 490
CGCGCATGCGCAAGATCTTCAGCCGGCTCATCTACATCGCGCAGTCCAAAGGTGCTTGGATTCTCACGGG 560
AGGCACCCATTATGGCCTGACGAAAGTACATCGGGGAGGTGGTGAGAGATAACACCATCAGCAGGAGTTCA 630
GAGGAGAAATATTGTGGCCATTGGCATAAGCAGCTGGGGCATGGTCTCCAACCGGGAACCCCTCATCAGGA 700

710 720 730 740 750 760 770

ATTGCGATGCTGAGGGCTATTTTTTAGCCCAAGTACCTTAAGATGACTTCACAAGGGATCCACTGTATAT 770
CCTGGACAACAACACACACATTTGGCTGCTCGTGGACAAAGGCTGTATGGACATCCCACTGTGCAAGCA 840
AAGCTCCGGAAATCAGCTAGAGAAAGCATATCTGTGAGCGCACTATTCAAGATTCCAACTATGGTGGCAAGA 910
TCCCCATTGTGTGTTTGGCCCAAGGAGGTGGAAAAGAGACTTTGAAAGCCATCAATACCTCCATCAAAAA 980
TAAATTTCTTGTGTGGTGGTGGAAAGGCTCGGGCGGATCGGTGATGTGATCGCTAGCCTGGTGGAGGTG 1050

1060 1070 1080 1090 1100 1110 1120

GAGGATGCCCGGACATCTTTTGGCGTCAAGGAGAAGGTGGTGGGCTTTTTACCCCGGACGGTGTCCGGG 1120
TGTCTGAGGAGGAGACTGAGAGTTGGATCAAAATGGGTCAAAAGAAATTCTCGAATGTTCTCACCTATTAA 1190
AGTTATTAAGAAATGGAAGAAGCTGGGGATGAAATTTGTAGCAATGGCATCTCTACGGCTATACAAAGCC 1260
TTCAGCACCAAGTGAGCAAGACAAAGGATAACTGGAATGGGCAGTGAAGCTTCTGTGGAGTGGAAACAGC 1330
TGGACTTAGCCAAATGATGAGATTTTCACCAATGACCGCGGATGGGAGTCTGCTGACCTTCAAGAAATCAT 1400

1410 1420 1430 1440 1450 1460 1470

GTTTACGGCTCTCATAAAGGACAGACCCAAGTTTGTGGGCTCTTTTCTGGAGAATGGCTTGAACCTACGG 1470
AAGTTTCTCACCCATGATGTCTCACTGAAGCTCTCTCCAACCACTTCAGCACGCTTGTGTACCGGAATC 1540
TGCAGATCGCCAAGAATTTCTATAATGATGCCCTCTTCACGTTTGTGTGGAAACTGGTTGCGAATTTCCG 1610
AAGAGGCTTCCGGAAAGGAAGACAGAAATGGCGGGGATGAGATGGACATAGAATCCACGACGTGTCTCT 1680
ATTACTCGGCACCCCTGCAAGCTCTCTTCATCTGGGCCATTTCTTCAGAAAGGAAGGAATCTTCCAAG 1750

1760 1770 1780 1790 1800 1810 1820

TCATTTGGGAGCAGACCCAGGGGCTGCACTCTGGCAGCCCTGCGAGCCAGCAAGCTTCTGAAGACTCTGGC 1820
CAAAATGAAGAAACACATCAATGCTGTGTGGGAGTTCGAGGAGCTGGCTAATGAGTACGAGACCCGGGT 1890
GTTGAGCTGTTCAGTGTGTACAGCAGCGATGAAGACTTGGCAGAACAGCTGCTGGTCTATTCTGTG 1960
AAGCTTGGGGTGGAAAGCAACTGTCTGGAGCTGGGGTGGAGGCTACAGACCAAGCATTCACCGGCCAGCC 2030
TGGGGTCCAGAAATTTCTTTCTAAGCAATGGATGGAGAGATTTCCCGAGACACCAAGAAGCTGGAGATT 2100

Fig. 12A (i)

002150-002650

2110 2120 2130 2140 2150 2160 2170
TCCTGTGTCTGTTTATTATACCCCTTGGTGGGCTGTGGCTTTGTATCATTTAGGAAGAAACCTGTGACA 2170
AGCACAAGAAGCTGCTTTGGTACTATGTGGGCTCTTCCACCTCCCCCTTCGTGGTCTTCTCCTGGAATGT 2240
GGTCTTCTACATCGCCTTCTCTGCTGTTTGGCTACGTGCTGCTCATGGATTTCATTTCGGTGCCACAC 2310
CCCCCGAGCTGCTCCTGTAATCCCTGGTCTTTGTCTCTTCTGTGATGAAGTCAGACAGTGGTACGTAA 2380
ATGGGGTGAATTATTTTACTGACCTGTGGAATGTGATGGACACGCTGGGGCTTTTTTACTTCATAGCAGG 2450
2460 2470 2480 2490 2500 2510 2520
AATTGTATTTGGGCTCCACTCTTCTAATAAAAGCTCTTTGTATTCTGGACGAGTCATTTTCTGTCTGGAC 2520
TACATTATTTTCACTCTAAGATTGATCCACATTTTACTGTAAGCAGAAACTTAGGACCCAAGATTATAA 2590
TGCTGCAGAGGAIGCTGATCGATGTGTCTTCTCTCTCTCTCTTTGC3GTGTGGATGGTGGCCTTTGG 2660
CGTGGCCAGGCAAGGGATCCTTAGGCAGAAATGAGCAGCGCTGGAGGTGGATATTCGTTTCGGTCATCTAC 2730
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2810 2820 2830 2840 2850 2860 2870
GCACCTTCACTGGGAATGAGTCCAAGCCACTGTGTGTGGAGCTGGATGAGCACAACCTGCCCGGTTCCC 2870
CGAGTGGATCACCATCCCCCTGGTGTGCATCTACATGTTATCCACCAACATCCTGCTGGTCAACCTGCTG 2940
GTCGCCATGTTTGGCTACACGGTGGGCACCGTCCAGGAGAAACAATGACCAGGTCTGGAAGTTCAGAGGT 3010
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CATGGTGTGTGAAGAAGTGCCTCAAGTGTGGTGCAGGAGAAACATGGAGTCTTCTGTCTGTGTTTTC 3150
3160 3170 3180 3190 3200 3210 3220
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CAAGGGTCTTCTGAAAGAGATTGCTAATAAAATCAAAATAAACTGTATGAACTCTAATGGAGAAAAATC 3360
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3510 3520 3530 3540 3550 3560 3570
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GCTGTCTTCTCTCTGTGTCTCAATGGCTGGGACTGGA3GTTGATAGTTTAAGTGTGTTCTTACCGCCTCC 3640
TTTTTCTTTTAACTCTTATTTTGAATGAACACAATAATAGGAGAACATCTATCCTATGAAATAAGAACCTGG 3710
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3860 3870 3880 3890 3900 3910 3920
AAGAGGACCCCGCTCTCTTTCAGGAAAAAGTGTCTTCAATTTCTCAGGATGCTTCTTACCTGTGAGAGGAGGT 3920
GACAAGGCAGTCTCTTGTCTCTTGGACTCAGCAGGCTCCTATTGAAGGAACACCCCAATTCCTAAATA 3990
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GAACATAAATTTGCCCCATTACCTTAAGTAAATCACTGCTAACAATTTCTGGATGGTTTTTCAAGTCTAT 4200
4210 4220 4230 4240 4250 4260 4270
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TTGATCATTTGGGATGAGCACTCTTGTGCGATGAATCCTATTGCTGTATTTGGGAAAAATTTTCCAAAGGTTAC 4480
ATTCCAATAAATACTATTTATTATTAATAATTAATAATATCGATTTATTATTAAAAACCAATTTATAAGGCT 4550

Fig. 12A(2)

4560	4570	4580	4590	4600	4610	4620
TTTTCATAAATGTATAGCAAAATAGGAATTATTAACCTTGAGCATAAGATATGAGATACATGAACCTGAACT 4620						
ATTAATAATAAATATTATATTTAACCCTAGTTTAAGAAGAAGTCAATATGCTTATTTAAATATTATGGAT 4690						
GGTGGGCAGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGCAAAACCACATCTCTACT 4760						
AAAAATAAAAAAATAGCTGGGTGTGGTGGTGCCTCCTGTAATCCCAGCTACTCAGAAGGCTGAGGTAC 4830						
AAGAATTGCTGGAACCTGGGAGGCGGAGGTTGCAGTGAACCAAGATTGCACCACTGCACTCCAGCCGGGG 4900						
4910	4920	4930	4940	4950	4960	4970
TGACAGAGTGAGACTCCGACTGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAATTATGG 4970						
ATGGTGAAGGGAATGGTATAGAATTGGAGAGATTATCTTACTGAACACCTGTAGTCCCAGCTTTCTCTGG 5040						
AAGTGGTGGTATTTGAGCAGGATGTGCACAAGGCAATTGAAATGCCATAATTAGTTTCTCAGCTTTGAA 5110						
TACACTATAAACTCAGTGGCTGAAGGAGGAAAATTTAGAAGGAAGCTACTAAAAGATCTAATTTGAAAAA 5180						
CTACAAAAGCATTAACTAAAAAAGTTTATTTTCCTTTTGTCTGGGCAGTAGTGAAAATAAATACTACTCACA 5250						
5260	5270	5280	5290	5300	5310	5320
CATTCACTATGTTTGCAAGGAATTAACACAAATAAAGATGCCCTTTTACTTAAACGCCAAGACAGAAAA 5320						
CTTGCCCAATACTGAGAAGCAACTTGCATTAGAGAGGGAAGTGTAAATGTTTTCAACCCAGTTTCATCTG 5390						
GTGGAATGTTTTTGCAGGTACTCTGAGAATTTTGCCTATGAAAAATCATTATTTTGTAGTGTAGTTTCAAA 5460						
TAATGTATTGAACATACTTCTAATCAAAGGTGCTATGTCCTGTGTATGGTACTAAATGTGTCTCTGTGTA 5530						
CTTTTGCACAACCTGAGAAATCCTGCGGCTTGGTTTAAATGAGTGTGTTTCATGAAATAAATAATGGAGGAAT 5600						
5610	5620	5630	5640	5650	5660	5670
GTCAAA 5668						

Fig. 12A(3)

10 20 30 40 50 60 70

MRNRRNDTLOSTRTRYSSASRSTDSYSESDLVNFIQANFKKRECVFSTKDSKAPENVCKCGYAQSQHME 70
 GTQINQSEKWNYYKKHTKEFPTDAFGDIQFETLGKKGKYIRLSCOTDAEILYELLTQHWHLKTPLNLVISVT 140
 GGAKNFALKPRMRKIFSRLLIYIAQSKGAWILTGGTHYGLTKYIGEVRONTISRSEENIVAIGIAAWGM 210
 VSNROTLIRNCOAEGYFLAQYLMDOFTROPLYLONNHTHLLVDNGCHGHPTVEAKLRNQLKHKISERT 280
 IQDSNYGGKIPIVCFAQGGGKETLKAINTSINKKPCVVVEGSGRIADVIAASLVEVEDAPTSSAVKEKLV 350

360 370 380 390 400 410 420

RFLPRTVSRSLSEEETESWIKWLKEILECSHLLTVIKMEZAGDEIVSNAISYALYKAFSTSEQOKDNWNGQ 420
 LKLLLEWNCLOLANDEIFTNDRRWESAOLQEVMTALIKDRPKFVRLFLENGLNLRKFLTHOVLTELFN 490
 HFSTLVYRNLIKNSYNOCALLTFVWKLVANFRRGFRKEDRNGRDEMIELHGVSPITRHPLQALFIWAI 560
 LONKKELSKVIWEGTRGCTLAALGASKLLKTLAKVKNDINAAGESEELANEYFTRAVELFTECYSSOEDL 630
 AEQLLVYSCEAWGGSNCLELAVEATDQHFTAQPGVQNFLSKQWYGEISROTKNWKIILCLFIIPLVGCGF 700

710 720 730 740 750 760 770

VSFRKKPVCKHKKLLWYYYVAFFTSPFVVFVSWNVVFYIAFLLLFAYVLLMDGFHSVPHPELVLYSLVFVLF 770
 CDEVROWYVNGVNYFTDLWNVMDTLGLFYFIAGIVFRHSSNKSSLYSGRYIFCLDYIFTLRLTHFTV 840
 SRNLGPKIIMLQMLIDVFFFLFLFAYVMVAFGVARGGILRQNECRWRWIFRSVIYEPYLA MFQGVPSOV 910
 DGTTYDFAHCTFTGNESKFLCVELDEHNLPRFPENITIPLYCIYMLSTNILLVYNLLVAMFGYTVGTVCEN 980
 NDCVWKFGRYFLVQEYCSRLNIPFPFIVFAYFYMVKKCFKCCCKEKNMESSVCCFKNEDNETLAWEGVM 1050

1060 1070 1080 1090 1100 1110 1120

IKENYLVKINTKANDTSEEMRHRFRQLDTKLNCLKGGLKEIANKIK. 1096

002793-062600

Fig. 12B